

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- Sub B1*
- (i) APPLICANT: Thomas Ciossek, Axel Ullrich, Birgit Millauer
- (ii) TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF MDK1 SIGNAL TRANSDUCTION DISORDERS
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 90071
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
(B) COMPUTER: IBM compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)  
(D) SOFTWARE: WordPerfect (Version 5.1)
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: to be assigned  
(B) FILING DATE: January 3, 1995  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- Prior applications total,  
including application  
described below: none
- (A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Warburg, Richard J.  
(B) REGISTRATION NUMBER: 32,327  
(C) REFERENCE/DOCKET NUMBER: 208/007

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600  
(B) TELEFAX: (213) 955-0440  
(C) TELEX: 67-3510

## (1) INFORMATION FOR SEQUENCE ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4304  
(B) TYPE: nucleic acid  
(C) STRANDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50  
CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100  
GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150  
TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG 200  
CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250  
TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300  
CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350  
CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA 400  
GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATAACAGGT 450  
GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500  
TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG 550  
AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAAGTTGCA AGGAAACGTT 600  
TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650  
AAAACCTTTA TGTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700  
CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750  
GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG 800  
GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG 850

B-Sub

ACCATTGTTG	AGAACTTAGC	TGTCTTTCCA	GATACAGTGA	CTGGTTCGGA	900
ATTTTCCTCC	TTAGTCGAGG	TCCGTGGGAC	ATGTGTCAGC	AGTGCCGAGG	950
AAGAGGCAGA	AAATTCCCCC	AGAATGCATT	GCAGTGCAGA	AGGAGAGTGG	1000
CTAGTACCCA	TTGGAAAATG	CATCTGCAAA	GCAGGCTATC	AGCAAAAAGG	1050
GGACACTTGC	GAACCCTGTG	GCCGCAGGTT	CTACAAATCT	TCCTCTCAGG	1100
ATCTCCAGTG	TTCTCGTTGT	CCAACCCACA	GCTTCTCTGA	CCGAGAAGGA	1150
TCATCCAGGT	GTGAATGTGA	AGATGGGTAC	TACAGAGCTC	CTTCTGATCC	1200
ACCATACGTT	GCATGCACGA	GGCCTCCCTC	TGCACCACAG	AACCTTATTT	1250
TCAATATCAA	TCAAACGACT	GTAAGTTTGG	AATGGAGTCC	TCCGGCTGAC	1300
AACGGGGGAA	GAAACGATGT	CACCTACAGA	ATACTGTGTA	AGCGGTGCAG	1350
TTGGGAACAG	GGAGAATGTG	TGCCATGCGG	AAGTAACATT	GGATACATGC	1400
CCCAGCAGAC	GGGATTAGAG	GATAACTATG	TCACTGTCAT	GGACCTACTT	1450
GCCCATGCAA	ATTACACTTT	CGAAGTTGAA	GCTGTAAATG	GAGTTTCGGA	1500
CTTAAGCAGA	TCCCAGAGGC	TCTTCGCTGC	TGTTAGCATC	ACCACCGGTC	1550
AAGCAGCTCC	CTCGCAAGTG	AGTGGAGTCA	TGAAGGAGCG	AGTACTGCAG	1600
CGGAGTGTGC	AGCTTTCCTG	GCAGGAGCCG	GAGCATCCCA	ATGGAGTCAT	1650
CACGGAATAT	GAAATCAAGT	ATTATGAGAA	AGATCAACGG	GAAAGGACGT	1700
ACTCAACACT	CAAAACCAAG	TCCACCTCCG	CCTCCATTAA	TAATCTGAAA	1750
CCGGGAACAG	TGTACGTCTT	TCAGATCCGG	GCGGTCACTG	CTGCCGGTTA	1800
TGGAAACTAC	AGCCTAGGC	TTGATGTTGC	CACACTTGAG	GAAGCTTCAG	1850
GTAAAATGTT	TGAAGCGACA	GCAGTCTCCA	GTGAACAGAA	TCCTGTCATC	1900
ATAATTGCTG	TAGTGGCTGT	AGCAGGGACC	ATCATCTTGG	TGTTTCATGGT	1950
GTTCGGCTTC	ATCATTGGAA	GAAGGCACTG	TGGTTATAGC	AAGGCTGACC	2000
AAGAAGGGGA	TGAAGAACTC	TACTTTCATT	TTAAATTTCC	AGGCACCAAA	2050
ACCTACATTG	ACCCTGAAAC	CTATGAGGAC	CAAATAGAG	CTGTCCATCA	2100
ATTCGCCAAG	GAGCTAGATG	CCTCCTGTAT	TAAAATTGAG	CGTGTGATTG	2150
GTGCAGGAGA	ATTTGGAGAA	GTTTGCAGTG	GTCGTTTGAA	ACTTCCGGGC	2200
CAGAGAGATG	TTGCAGTGGC	CATAAAAACC	CTGAAAGTTG	GTTACACAGA	2250

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B1

AAAGCAAAGG	AGGGACTTTT	TATGCGAAGC	AAGCATCATG	GGGCAATTG	2300
ACCACCCAAA	TGTCGTCCAT	TTGGAAGGGG	TTGTTACAAG	AGGGAAGCCT	2350
GTCATGATTG	TGATAGAGTT	CATGGAGAAT	GGAGCCCTGG	ATGCATTTCT	2400
CAGGAAACAC	GATGGGCAGT	TTACAGTCAT	TCAGTTGGTA	GGAATGTTGA	2450
GAGGTATTGC	CGCTGGGATG	CGATACTTGG	CTGATATGGG	ATACGTTTAC	2500
AGGGACCTTG	CAGCGCGCAA	CATCCTTGTC	AACAGCAATC	TTGTTTGTA	2550
AGTGTGAGAT	TTTGGCCTTT	CCCGGGTTAT	AGAGGATGAT	CCCGAAGCTG	2600
TCTACACCAC	GACTGGTGGA	AAAATTCCAG	TAAGGTGGAC	TGCACCGGAA	2650
GCCATTCAAT	ACCGGAAGTT	CACCTCAGCC	AGCGATGTGT	GGAGCTATGG	2700
GATTGTGATG	TGGGAAGTGA	TGTCTTATGG	AGAAAGACCT	TACTGGGACA	2750
TGTCAAATCA	AGATGTCATT	AAAGCGATAG	AAGAAGGTTA	TCGTTTGCCG	2800
GCGCCCATGG	ATTGCCCAGC	TGGTCTTCAC	CAGCTAATGC	TGGATTGTTG	2850
GCAGAAAGAT	CGGGCGGAAA	GGCCAAAGTT	TGAGCAGATA	GTCGGAATTC	2900
TAGACAAAAT	GATTCGAAAC	CCAAGTAGTC	TGAAAACACC	CCTGGGAACT	2950
TGTAGTAGAC	CCTTAAGCCC	TCTTCTGGAC	CAGAGCACTC	CTGACTTCAC	3000
TGCCTTCTGT	TCAGTTGGAG	AATGGTTGCA	AGCTATTAAA	ATGGAAAGGT	3050
ATAAGGACAA	CTTCACAGCA	GCGGGTTACA	ACTCACTCGA	GTCAGTGGCC	3100
AGGATGACTA	TCGATGATGT	GATGAGTTTA	GGGATCACAC	TGGTTGGCCA	3150
TCAAAGAAG	ATCATGAGCA	GCATCCAGAC	TATGCGGGCA	CAAATGTTGC	3200
ATTTACACGG	AACAGGCATC	CAAGTGTGAC	ACATCGGCCT	CCCTCAGATG	3250
AGGCTTAAGA	CTGCAGGAGA	ACAGTTCTGG	CCTTCAGTAT	ACGCATAGAA	3300
TGCTGCTAGA	AGACAGTTGA	TATACTGGGT	CCTTCCTACA	AGAAAGAGAA	3350
GATTTTAGAA	GCACCTCCAG	ACTTGAAGTC	CTAAGTGCCA	CCAGAATATA	3400
CAAAAAGGGA	ATTTAGGATC	CACCACTGGT	GGCCAGGAAC	ACAGCAGAGA	3450
CAATAAACAA	AGTACTACCT	GAAAAACATC	CCAACACCTT	GAGCTCTCGA	3500
ACCTCCTTTT	TATCTTATAG	ACTTTTTTAA	AATGTACATA	AAGAATTTAA	3550
GAAAGAATAT	ATTTGTCAAA	TAAAAATCAT	GATCTTATTG	TTAAAATCAA	3600
TGAAATATTT	TCCTTAAAAT	ATGTGATTTT	AGACTATTCT	TTCCAGAAC	3650

CATCTGTGTT TATTCTGCTT AAGGACTTTG TTTTAGAAAG TTATTTGTAG 3700  
 CTTTGGACCT TTTTAGTGTT AAATTTATGA CACGTTACTA CACTGGGAAC 3750  
 CTTTGAAGAC TCTCAAACCT AAAGGAAAGC AAAACTACGC ACATAGTCGA 3800  
 GGATGGACTT TGTCTTCAT GGCTTTGGTA TCCTGGCTGT GTCATTTTGT 3850  
 TAAACCAGTG ATGTTTTTCAT ATTGTTTGCT GATTGGCAGG TAGTTCAAAA 3900  
 TTGCAAGTTG CCAAGAGCTC TGATATTTTT TAACAGGATT TTTTTTCTT 3950  
 TGTAAAAATC AGATAACATA CTAACCTTTC AATGAAAAA AAAAAAAAAG 4000  
 AAGCAATAAT GATCCATAAA TACTATAAGG CACTTTTAAC AGATTGTTTA 4050  
 TAGAGTGATT TACTAGGCAG AATTTAATAA AAAAAAAGA GAGATGTCAA 4100  
 ATTTTAGGTT TATGTGTATA TGATAAAAGG CTGAGCTTCG TCTGAAGATG 4150  
 CTGGTGAAAG CAAGACTGGA AGCGAAGCTC TCCAGCTTTG GCTAACCCAA 4200  
 TCCGAGCACA TCAAGAGCTT CAGTCTTG TG ACAGTAAGAA ATTTAGGAAC 4250  
 ATAGTTGACC TATATTTTGT ATTCTTTCTT GTTGAATGCA GTCCAAATAC 4300  
 AAAA 4304

(1) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 998  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile  
 1 5 10 15  
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu  
 20 25 30  
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile  
 35 40 45

Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn  
 50 55 60  
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn  
 65 70 75 80  
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln  
 85 90 95  
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu  
 100 105 110  
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr  
 115 120 125  
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val  
 130 135 140  
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu  
 145 150 155 160  
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro  
 165 170 175  
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys  
 180 185 190  
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile  
 195 200 205  
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe  
 210 215 220  
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu  
 225 230 235 240  
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp  
 245 250 255  
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys  
 260 265 270  
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser  
 275 280 285  
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg  
 290 295 300  
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro  
 305 310 315 320

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Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln  
 325 330 335  
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser  
 340 345 350  
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu  
 355 360 365  
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser  
 370 375 380  
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val  
 385 390 395 400  
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu  
 405 410 415  
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala  
 420 425 430  
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly  
 435 440 445  
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln  
 450 455 460  
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr  
 465 470 475 480  
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys  
 485 490 495  
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val  
 500 505 510  
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro  
 515 520 525  
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu  
 530 535 540  
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val  
 545 550 555 560  
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe  
 565 570 575  
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly  
 580 585 590  
 Asp Glu Glu Leu Tyr Phe His Phe Lys Phe Pro Gly Thr Lys Thr Tyr  
 595 600 605

Ile Asp Pro Glu Thr Tyr Glu Asp Pro Asn Arg Ala Val His Gln Phe  
 610 615 620  
 Ala Lys Glu Leu Asp Ala Ser Cys Ile Lys Ile Glu Arg Val Ile Gly  
 625 630 635 640  
 Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Leu Pro Gly  
 645 650 655  
 Gln Arg Asp Val Ala Val Ala Ile Lys Thr Leu Lys Val Gly Tyr Thr  
 660 665 670  
 Glu Lys Gln Arg Arg Asp Phe Leu Cys Glu Ala Ser Ile Met Gly Gln  
 675 680 685  
 Phe Asp His Pro Asn Val Val His Leu Glu Gly Val Val Thr Arg Gly  
 690 695 700  
 Lys Pro Val Met Ile Val Ile Glu Phe Met Glu Asn Gly Ala Leu Asp  
 705 710 715 720  
 Ala Phe Leu Arg Lys His Asp Gly Gln Phe Thr Val Ile Gln Leu Val  
 725 730 735  
 Gly Met Leu Arg Gly Ile Ala Ala Gly Met Arg Tyr Leu Ala Asp Met  
 740 745 750  
 Gly Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser  
 755 760 765  
 Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Ile Glu  
 770 775 780  
 Asp Asp Pro Glu Ala Val Tyr Thr Thr Thr Gly Gly Lys Ile Pro Val  
 785 790 795 800  
 Arg Trp Thr Ala Pro Glu Ala Ile Gln Tyr Arg Lys Phe Thr Ser Ala  
 805 810 815  
 Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr  
 820 825 830  
 Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala  
 835 840 845  
 Ile Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Asp Cys Pro Ala Gly  
 850 855 860  
 Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Asp Arg Ala Glu Arg  
 865 870 875 880  
 Pro Lys Phe Glu Gln Ile Val Gly Ile Leu Asp Lys Met Ile Arg Asn  
 885 890 895



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Pro Ser Ser Leu Lys Thr Pro Leu Gly Thr Cys Ser Arg Pro Leu Ser  
 900 905 910  
 Pro Leu Leu Asp Gln Ser Thr Pro Asp Phe Thr Ala Phe Cys Ser Val  
 915 920 925  
 Gly Glu Trp Leu Gln Ala Ile Lys Met Glu Arg Tyr Lys Asp Asn Phe  
 930 935 940  
 Thr Ala Ala Gly Tyr Asn Ser Leu Glu Ser Val Ala Arg Met Thr Ile  
 945 950 955 960  
 Asp Asp Val Met Ser Leu Gly Ile Thr Leu Val Gly His Gln Lys Lys  
 965 970 975  
 Ile Met Ser Ser Ile Gln Thr Met Arg Ala Gln Met Leu His Leu His  
 980 985 990  
 Gly Thr Gly Ile Gln Val  
 995

## (1) INFORMATION FOR SEQUENCE ID NO: 3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 610  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile  
 1 5 10 15  
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu  
 20 25 30  
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile  
 35 40 45  
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn  
 50 55 60  
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn  
 65 70 75 80

Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln  
 85 90 95  
 Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu  
 100 105 110  
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr  
 115 120 125  
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val  
 130 135 140  
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu  
 145 150 155 160  
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro  
 165 170 175  
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys  
 180 185 190  
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile  
 195 200 205  
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe  
 210 215 220  
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu  
 225 230 235 240  
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp  
 245 250 255  
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys  
 260 265 270  
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser  
 275 280 285  
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg  
 290 295 300  
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro  
 305 310 315 320  
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln  
 325 330 335  
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser  
 340 345 350  
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu  
 355 360 365

Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser  
 370 375 380  
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val  
 385 390 395 400  
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu  
 405 410 415  
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala  
 420 425 430  
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly  
 435 440 445  
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln  
 450 455 460  
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr  
 465 470 475 480  
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys  
 485 490 495  
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val  
 500 505 510  
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro  
 515 520 525  
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu  
 530 535 540  
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val  
 545 550 555 560  
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe  
 565 570 575  
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly  
 580 585 590  
 Asp Glu Glu Leu Tyr Phe His Ser Leu Val Thr Asn Glu His Leu Ser  
 595 600 605  
 Val Leu  
 610

## (1) INFORMATION FOR SEQUENCE ID NO: 4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2901  
(B) TYPE: nucleic acid  
(C) STRANDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50  
CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100  
GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150  
TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG 200  
CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250  
TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300  
CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350  
CACAACAAAC AGAATTGGAA TGGATTTCTT CTCCACCCAG TGGGTGGGAA 400  
GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATAACAGGT 450  
GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500  
TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG 550  
AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAAGTTGCA AGGAAACGTT 600  
TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650  
AAAACCTTTA TGTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700  
CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750  
GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG 800  
GGGCTTGCAAT AGCATTGGTT TCTGTCAAAG TGTACTACAA GAAGTGCTGG 850  
ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA 900  
ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG 950  
AAGAGGCAGA AAATTCCTCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG 1000  
CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG 1050

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B1

GGACACTTGC	GAACCCTGTG	GCCGCAGGTT	CTACAAATCT	TCCTCTCAGG	1100
ATCTCCAGTG	TTCTCGTTGT	CCAACCCACA	GCTTCTCTGA	CCGAGAAGGA	1150
TCATCCAGGT	GTGAATGTGA	AGATGGGTAC	TACAGAGCTC	CTTCTGATCC	1200
ACCATACGTT	GCATGCACGA	GGCCTCCCTC	TGCACCACAG	AACCTTATTT	1250
TCAATATCAA	TCAAACGACT	GTAAGTTTGG	AATGGAGTCC	TCCGGCTGAC	1300
AACGGGGGAA	GAAACGATGT	CACCTACAGA	ATACTGTGTA	AGCGGTGCAG	1350
TTGGGAACAG	GGAGAATGTG	TGCCATGCGG	AAGTAACATT	GGATACATGC	1400
CCCAGCAGAC	GGGATTAGAG	GATAACTATG	TCACTGTGAT	GGACCTACTT	1450
GCCCATGCAA	ATTACACTTT	CGAAGTTGAA	GCTGTAAATG	GAGTTTCGGA	1500
CTTAAGCAGA	TCCCAGAGGC	TCTTCGCTGC	TGTTAGCATC	ACCACCGGTC	1550
AAGCAGCTCC	CTCGCAAGTG	AGTGGAGTCA	TGAAGGAGCG	AGTACTGCAG	1600
CGGAGTGTGC	AGCTTTCCTG	GCAGGAGCCG	GAGCATCCCA	ATGGAGTCAT	1650
CACGGAATAT	GAAATCAAGT	ATTATGAGAA	AGATCAACGG	GAAAGGACGT	1700
ACTCAACACT	CAAAACCAAG	TCCACCTCCG	CCTCCATTAA	TAATCTGAAA	1750
CCGGGAACAG	TGTACGTCTT	TCAGATCCGG	GCGGTCACTG	CTGCCGGTTA	1800
TGGAAACTAC	AGCCCTAGGC	TTGATGTTGC	CACACTTGAG	GAAGCTTCAG	1850
GTAAAATGTT	TGAAGCGACA	GCAGTCTCCA	GTGAACAGAA	TCCTGTCATC	1900
ATAATTGCTG	TAGTGGCTGT	AGCAGGGACC	ATCATCTTGG	TGTTTCATGGT	1950
GTTCGGCTTC	ATCATTEGAA	GAAGGCACTG	TGGTTATAGC	AAGGCTGACC	2000
AAGAAGGGGA	TGAAGAACTC	TACTTTCATT	CTTTAGTAAC	AAATGAGCAC	2050
CTGTCAGTTT	TATAAACCGC	AACAATAACT	GTTTAAGACA	ATCAATTTTG	2100
GATAAACAAAT	CAACTACAGC	AGAATAAATC	AAGATTTTAA	AGTCCCATT	2150
TCCTTTATAC	ATTCTGCTTA	TTTTGTTGTT	ATATGTTTAT	TTTTTAAACT	2200
CTGATCTTGA	TTGAATGTGA	TACCATAAGC	ACAGTTAGGC	TGCAGTGTA	2250
ATATATAAAG	ACATTGTTCT	GAGAGCAGTA	CGATTTTCATG	GAAAGATTGT	2300
TTGGTGCTT	TGTTAAAATT	AATAAAGAAT	TTTAAAGGAT	ATAGTGTAAT	2350
TTTCTTCATT	GCATTAATAT	AACCAAATAT	GCCTACCTAT	CTTTGTCTTG	2400
AACCAAATGA	ATAGATTGTTG	AATACTTTAT	TGTAATTGAA	TTTGATATAA	2450

AGTTGACTGA GCATTTATGT GTTACCTGCA TGCTTCTGGG TGCATTGAAA 2500  
 TATTTTAACT TTAAAAATGA TACTATGTTG TTTCAATTTT GACTACCTTT 2550  
 TGTGAGGCAT ACTGGCTACC TCCTCCTATT AGCTAAGATC TTCCAAAGCC 2600  
 TTATAATGAA AAGTTTATAT AAACCATTTC TCTTTCAAAT CACTGTCATA 2650  
 CTTGGTCACG GATCCCAGGA ATATTGTAAA TTTTCTAATT TACTCTGCAC 2700  
 TTTGTATATC CAGCCTCTAT TACCCTCAAG GTGAATATAA AACTATGTCT 2750  
 TTTGAATATT TCTCTTTGAT TTTGTGATAG CAGTCCCTCA TATCTTGAC 2800  
 TAATTTTATG TATATGTCAA CAGTGGTTGG TCTTTAAAAA TAAATCAAAG 2850  
 AATAAGTAAA AAAAAAAAAA AAAAAAAAAA AAAAATAAAA AAAAAAAAAA 2900  
 A 2901

(1) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626  
 (B) TYPE: amino acid  
 (C) STRANDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Met Val Val Gln Thr Arg Phe Pro Ser Trp Ile Ile Leu Cys Tyr Ile  
 1 5 10 15  
 Trp Leu Leu Gly Phe Ala His Thr Gly Glu Ala Gln Ala Ala Lys Glu  
 20 25 30  
 Val Leu Leu Leu Asp Ser Lys Ala Gln Gln Thr Glu Leu Glu Trp Ile  
 35 40 45  
 Ser Ser Pro Pro Ser Gly Trp Glu Glu Ile Ser Gly Leu Asp Glu Asn  
 50 55 60  
 Tyr Thr Pro Ile Arg Thr Tyr Gln Val Cys Gln Val Met Glu Pro Asn  
 65 70 75 80  
 Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Lys Gly Asn Ala Gln  
 85 90 95

Arg Ile Phe Val Glu Leu Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu  
 100 105 110  
 Pro Gly Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr  
 115 120 125  
 Glu Thr Asp Tyr Asp Thr Gly Arg Asn Ile Arg Glu Asn Leu Tyr Val  
 130 135 140  
 Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Gly Asp Leu  
 145 150 155 160  
 Gly Glu Arg Lys Met Lys Leu Asn Thr Glu Val Arg Glu Ile Gly Pro  
 165 170 175  
 Leu Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys  
 180 185 190  
 Ile Ala Leu Val Ser Val Lys Val Tyr Tyr Lys Lys Cys Trp Thr Ile  
 195 200 205  
 Val Glu Asn Leu Ala Val Phe Pro Asp Thr Val Thr Gly Ser Glu Phe  
 210 215 220  
 Ser Ser Leu Val Glu Val Arg Gly Thr Cys Val Ser Ser Ala Glu Glu  
 225 230 235 240  
 Glu Ala Glu Asn Ser Pro Arg Met His Cys Ser Ala Glu Gly Glu Trp  
 245 250 255  
 Leu Val Pro Ile Gly Lys Cys Ile Cys Lys Ala Gly Tyr Gln Gln Lys  
 260 265 270  
 Gly Asp Thr Cys Glu Pro Cys Gly Arg Arg Phe Tyr Lys Ser Ser Ser  
 275 280 285  
 Gln Asp Leu Gln Cys Ser Arg Cys Pro Thr His Ser Phe Ser Asp Arg  
 290 295 300  
 Glu Gly Ser Ser Arg Cys Glu Cys Glu Asp Gly Tyr Tyr Arg Ala Pro  
 305 310 315 320  
 Ser Asp Pro Pro Tyr Val Ala Cys Thr Arg Pro Pro Ser Ala Pro Gln  
 325 330 335  
 Asn Leu Ile Phe Asn Ile Asn Gln Thr Thr Val Ser Leu Glu Trp Ser  
 340 345 350  
 Pro Pro Ala Asp Asn Gly Gly Arg Asn Asp Val Thr Tyr Arg Ile Leu  
 355 360 365  
 Cys Lys Arg Cys Ser Trp Glu Gln Gly Glu Cys Val Pro Cys Gly Ser  
 370 375 380

Sub  
 B1  
 Asn Ile Gly Tyr Met Pro Gln Gln Thr Gly Leu Glu Asp Asn Tyr Val  
 385 390 395 400  
 Thr Val Met Asp Leu Leu Ala His Ala Asn Tyr Thr Phe Glu Val Glu  
 405 410 415  
 Ala Val Asn Gly Val Ser Asp Leu Ser Arg Ser Gln Arg Leu Phe Ala  
 420 425 430  
 Ala Val Ser Ile Thr Thr Gly Gln Ala Ala Pro Ser Gln Val Ser Gly  
 435 440 445  
 Val Met Lys Glu Arg Val Leu Gln Arg Ser Val Gln Leu Ser Trp Gln  
 450 455 460  
 Glu Pro Glu His Pro Asn Gly Val Ile Thr Glu Tyr Glu Ile Lys Tyr  
 465 470 475 480  
 Tyr Glu Lys Asp Gln Arg Glu Arg Thr Tyr Ser Thr Leu Lys Thr Lys  
 485 490 495  
 Ser Thr Ser Ala Ser Ile Asn Asn Leu Lys Pro Gly Thr Val Tyr Val  
 500 505 510  
 Phe Gln Ile Arg Ala Val Thr Ala Ala Gly Tyr Gly Asn Tyr Ser Pro  
 515 520 525  
 Arg Leu Asp Val Ala Thr Leu Glu Glu Ala Ser Gly Lys Met Phe Glu  
 530 535 540  
 Ala Thr Ala Val Ser Ser Glu Gln Asn Pro Val Ile Ile Ile Ala Val  
 545 550 555 560  
 Val Ala Val Ala Gly Thr Ile Ile Leu Val Phe Met Val Phe Gly Phe  
 565 570 575  
 Ile Ile Gly Arg Arg His Cys Gly Tyr Ser Lys Ala Asp Gln Glu Gly  
 580 585 590  
 Asp Glu Glu Leu Tyr Phe His Ser Leu Tyr Arg Glu Arg Gly Asp Gly  
 595 600 605  
 Met Glu Lys Thr Gln His Asn Lys Lys Trp Met Ile Ala Ser Cys Ser  
 610 615 620  
 Arg Leu  
 625



## (1) INFORMATION FOR SEQUENCE ID NO: 6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2323  
(B) TYPE: nucleic acid  
(C) STRANDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: nucleic

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

AAGCGGCCGG TCTGCAGTCG GAGACTTGCA GGCAGCAAAC ACGGTGCGAA 50  
CGAACCGGAG GGGGGAGAGA GAAATCAAAC AGCTAAGCGT GGAGCAGACG 100  
GCCTGGGACC CAGAAGGGGA TCGATGCGAG GAGCGCAATA ATAACAACAA 150  
TAATAACCCA CTTCGGAGCA AACAGCATCT AAAGAGCTGC GACCCAACTG 200  
CAGCCTAAAA AAATCAAACC TGCTCATGCA CCATGGTTGT TCAAACCTCGG 250  
TTCCCTTCGT GGATTATTTT GTGTTACATC TGGCTGCTTG GCTTTGCACA 300  
CACGGGGGAG GCGCAGGCTG CGAAGGAAGT ACTATTACTG GACTCGAAAG 350  
CACAACAAAC AGAATTGGAA TGGATTTCCT CTCCACCCAG TGGGTGGGAA 400  
GAAATTAGTG GTTTGGATGA GAACTACACT CCGATAAGAA CATAACAGGT 450  
GTGCCAGGTC ATGGAGCCCA ACCAGAACAA CTGGCTGCGG ACTAACTGGA 500  
TTTCTAAAGG CAACGCACAA AGGATTTTTG TAGAATTGAA ATTCACCTTG 550  
AGGGATTGTA ATAGTCTTCC CGGAGTCCTG GGAAGTTCGCA AGGAAACGTT 600  
TAATTTGTAC TATTATGAAA CAGACTACGA CACCGGCAGG AATATACGAG 650  
AAAACCTTTA TGTTAAAATA GACACCATTG CTGCAGATGA AAGTTTCACA 700  
CAAGGTGACC TTGGTGAAAG AAAGATGAAG CTGAACACTG AGGTGAGAGA 750  
GATTGGACCT TTGTCCAAAA AGGGATTCTA TCTTGCCTTT CAGGATGTAG 800  
GGGCTTGCAT AGCATTGGTT TCTGTCAAAG TGTAATACAA GAAGTGCTGG 850  
ACCATTGTTG AGAACTTAGC TGTCTTTCCA GATACAGTGA CTGGTTCGGA 900  
ATTTTCCTCC TTAGTCGAGG TCCGTGGGAC ATGTGTCAGC AGTGCCGAGG 950  
AAGAGGCAGA AAATCCCCC AGAATGCATT GCAGTGCAGA AGGAGAGTGG 1000  
CTAGTACCCA TTGGAAAATG CATCTGCAAA GCAGGCTATC AGCAAAAAGG 1050

*Sub*  
*B*

GGACACTTGC	GAACCCTGTG	GCCGCAGGTT	CTACAAATCT	TCCTCTCAGG	1100
ATCTCCAGTG	TTCTCGTTGT	CCAACCCACA	GCTTCTCTGA	CCGAGAAGGA	1150
TCATCCAGGT	GTGAATGTGA	AGATGGGTAC	TACAGAGCTC	CTTCTGATCC	1200
ACCATACGTT	GCATGCACGA	GGCCTCCCTC	TGCACCACAG	AACCTTATTT	1250
TCAATATCAA	TCAAACGACT	GTAAGTTTGG	AATGGAGTCC	TCCGGCTGAC	1300
AACGGGGGAA	GAAACGATGT	CACCTACAGA	ATACTGTGTA	AGCGGTGCAG	1350
TTGGGAACAG	GGAGAATGTG	TGCCATGCGG	AAGTAACATT	GGATACATGC	1400
CCCAGCAGAC	GGGATTAGAG	GATAACTATG	TCACTGTTCAT	GGACCTACTT	1450
GCCCATGCAA	ATTACACTTT	CGAAGTTGAA	GCTGTAAATG	GAGTTTCGGA	1500
CTTAAGCAGA	TCCCAGAGGC	TCTTCGCTGC	TGTTAGCATC	ACCACCGGTC	1550
AAGCAGCTCC	CTCGCAAGTG	AGTGGAGTCA	TGAAGGAGCG	AGTACTGCAG	1600
CGGAGTGTGC	AGCTTTCCTG	GCAGGAGCCG	GAGCATCCCA	ATGGAGTCAT	1650
CACGGAATAT	GAAATCAAGT	ATTATGAGAA	AGATCAACGG	GAAAGGACGT	1700
ACTCAACACT	CAAAACCAAG	TCCACCTCCG	CCTCCATTAA	TAATCTGAAA	1750
CCGGGAACAG	TGTACGTCTT	TCAGATCCGG	GCGGTCACTG	CTGCCGGTTA	1800
TGGAAACTAC	AGCCCTAGGC	TTGATGTTGC	CACACTTGAG	GAAGCTTCAG	1850
GTAAAATGTT	TGAAGCGACA	GCAGTCTCCA	GTGAACAGAA	TCCTGTCATC	1900
ATAATTGCTG	TAGTGGCTGT	AGCAGGGACC	ATCATCTTGG	TGTTCATGGT	1950
GTTCGGCTTC	ATCATTGGAA	GAAGGCACTG	TGGTTATAGC	AAGGCTGACC	2000
AAGAAGGGGA	TGAAGAACTC	TACTTTCATT	CTCTTTACAG	GGAAAGGGGA	2050
GACGGGATGG	AAAAGACACA	GCACAATAAG	AAGTGGATGA	TTGCATCGTG	2100
CTCTCGTTTTG	TAGGTCTCTT	TTCTTAATCA	ACACTATGAT	TTTGAAGTAC	2150
GCGTACACGA	AGCAAACGGG	AAGAGATAAG	GAATTAGCAT	TGTGAACCTG	2200
ACTGTAATCC	TCTCTTCCGG	AAAGAGATGA	GATGCTATTG	CGATGAGAAT	2250
GTACAACTTG	CACCTTGAAA	TCTTTTTTGA	TAATTAGTGC	TCAGGGGAGG	2300
GGGGGGGAAG	TAGAGAAAGC	AAA			2323

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala Ala Thr Ala Ala Ala  
5

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Ala Ala Thr Ala Ala Ala  
5

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

His Arg Asp Leu Ala Ala  
5

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

Sub  
B1

122

208/007

(A) LENGTH: 6  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 2 is valine or methionine; Xaa in position 5 is phenylalanine or tyrosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Asp Xaa Trp Ser Xaa Gly  
5